

WEST Search History

DATE: Sunday, May 05, 2002

Set Name Query side by side

Hit Count Set Name result set

DB=JPAB,EPAB,DWPI; PLUR=NO; OP=ADJ

L13 antibod\$3 and traf

15 L13

L12 C near traf

0 L12

DB=USPT; PLUR=NO; OP=ADJ

L11 L9 same antibod\$3

1 L11

L10 L9 same antibod?

0 L10

L9 C near traf

4 L9

L8 L6 and CD40

1 L8

L7 L6 and (I adj traf)

0 L7

L6 (tumor or tumour) adj necrosis adj factor adj receptor adj2 factor adj
6

1 L6

DB=JPAB,EPAB,DWPI; PLUR=NO; OP=ADJ

L5 L4 and (traf near I)

1 L5

L4 traf6 or (traf adj 6)

10 L4

DB=USPT; PLUR=NO; OP=ADJ

L3 L1 same (traf near I)

1 L3

L2 L1 with (traf near I)

1 L2

L1 traf6 or (traf adj 6)

36 L1

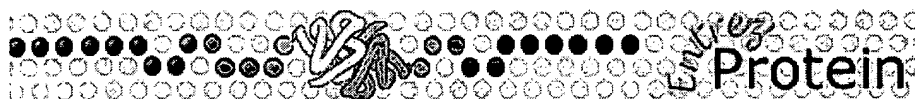
END OF SEARCH HISTORY

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS' ENTERED AT
17:31:47

ON 05 MAY 2002

L1 67 S TRAF(W)6
L2 0 S L1(S) (TRAF(A)I)
L3 0 S L1(S) (CAP(W) (I OR I))
L4 0 S L1(S) (CAP(W) (1 OR I))
L5 129 S CD(W)40
L6 303 S CD40(W)ASSOCIATED(W)PROTEIN OR (CAP(W)1)
L7 0 S L6(S) (I(A)TRAF)

=> s l1(s) tank



SEQ 27

Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Books	
Search	Protein	▼	for					Go	Clear
Limits		Preview/Index		History		Clipboard		Details	
Display	default	▼	Show:	20	▼	Send to	File	▼	Get Subsequence

☐ 1: Q93009. Ubiquitin carboxy...[gi:2501460][BLink](#), [Domains](#), [Links](#)

LOCUS Q93009 1102 aa linear PRI 15-SEP-2003
DEFINITION Ubiquitin carboxyl-terminal hydrolase 7 (Ubiquitin thiolesterase 7) (Ubiquitin-specific processing protease 7) (Deubiquitinating enzyme 7) (Herpesvirus associated ubiquitin-specific protease).
ACCESSION Q93009
VERSION Q93009 GI:2501460
DBSOURCE swissprot: locus UBP7_HUMAN, accession Q93009;
class: standard.
created: Nov 1, 1997.
sequence updated: Nov 1, 1997.
annotation updated: Sep 15, 2003.
xrefs: gi: [1545951](#), gi: [1545952](#), pdb accession 1NB8, pdb accession 1NBF
xrefs (non-sequence databases): MEROPSC19.016, GenewHGNC:12630, MIM [602519](#), GOGO:0005634, GOGO:0004197, GOGO:0004843, GOGO:0009405, InterProIPR002083, InterProIPR001394, PfamPF00917, PfamPF00443, SMARTSM00061, PROSITEPS50144, PROSITEPS00972, PROSITEPS00973, PROSITEPS50235
KEYWORDS Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family; Nuclear protein; 3D-structure.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 1102)
AUTHORS Everett,R.D., Meredith,M., Orr,A., Cross,A., Kathoria,M. and Parkinson,J.
TITLE A novel ubiquitin-specific protease is dynamically associated with the PML nuclear domain and binds to a herpesvirus regulatory protein
JOURNAL EMBO J. 16 (3), 566-577 (1997)
MEDLINE [97186723](#)
PUBMED [9034339](#)
REMARK SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Breast cancer
REFERENCE 2 (residues 1 to 1102)
AUTHORS Everett,R.D., Meredith,M., Orr,A., Cross,A., Kathoria,M. and Parkinson,J.
TITLE A novel ubiquitin-specific protease is dynamically associated with the PML nuclear domain and binds to a herpesvirus regulatory protein
JOURNAL EMBO J. 16 (7), 1519-1530 (1997)
MEDLINE [97277004](#)
PUBMED [9130697](#)
REMARK ERRATUM.
COMMENT -----
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[FUNCTION] CLEAVES UBIQUITIN FUSION PROTEIN SUBSTRATES. BINDS TO THE HERPES VIRUS PROTEIN VMW110 WHICH MAY THEREFORE MODULATE ITS SUBSTRATE SPECIFICITY OR ACTIVITY TO STABILIZE VIRAL PROTEINS.

[CATALYTIC ACTIVITY] Ubiquitin C-terminal thiolester + H(2)O = ubiquitin + a thiol.

[SUBCELLULAR LOCATION] NUCLEAR, PRESENT IN A MINORITY OF ND10 NUCLEAR BODIES. ASSOCIATION WITH VMW110 AT EARLY TIMES OF INFECTION LEADS TO AN INCREASED PROPORTION OF HAUSP-CONTAINING ND10.

[TISSUE SPECIFICITY] Widely expressed.

[SIMILARITY] Belongs to peptidase family C19.

[SIMILARITY] Contains 1 MATH domain.

FEATURES	Location/Qualifiers
source	1..1102 /organism="Homo sapiens" /db_xref="taxon:9606"
gene	1..1102 /gene="USP7" /note="synonym: HAUSP"
Protein	1..1102 /gene="USP7" /product="Ubiquitin carboxyl-terminal hydrolase 7" /EC_number="3.1.2.15"
Region	4..10 /gene="USP7" /region_name="Domain" /note="POLY-GLN."
Region	68..195 /gene="USP7" /region_name="Domain" /note="MATH."
Region	201 /gene="USP7" /region_name="Conflict" /note="H -> I (IN REF. 1; AA SEQUENCE)."
Region	205 /gene="USP7" /region_name="Conflict" /note="W -> P (IN REF. 1; AA SEQUENCE)."
Region	207 /gene="USP7" /region_name="Conflict" /note="S -> Q (IN REF. 1; AA SEQUENCE)."
Site	223 /gene="USP7" /site_type="active" /note="BY SIMILARITY."
Site	456 /gene="USP7" /site_type="active" /note="BY SIMILARITY."
Site	464 /gene="USP7" /site_type="active" /note="BY SIMILARITY."
Region	1066 /gene="USP7" /region_name="Conflict" /note="Q -> T (IN REF. 1; AA SEQUENCE)."

ORIGIN

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121 cnaesdstsw schaqavlki inyrddeksf srrishlffh kendwgfsnf mawsevt dpe
181 kgfiddkvvt fevfvdap hgvawdskkh tgyvglknqg atcymnsllq tlfftnqlrk
241 avymmp tegd dssksvplal qrvfyelqhs dkpvgtkklt ksfgwetlds fmqhdvqelc

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421 indrfefpeq lpldeflqkt dpkdpanyil havlvhsgdn hgghyvvyln pkgdgkwckf  
481 dddvvsrctk eeaiehnygg hdddlsvrhc tnaymlvyir esklsevlqa vtdhdipqql  
541 verlqeeekri eaqrkerqe ahlymqvqiv aedqfcghqg ndmydeekvk ytvfkvlkns  
601 slaefvqsls qtmgfpqdqi rlwpmqarsn gtrpamlnd eadgnktmie lsdnenpwti  
661 fletvdpela asgatlpkfd kdhdvmlflk mydpktrsln ycghiytpis ckirdllpvm  
721 cdragfiqdt slilyeekvp nlteriodyd vsldkaldel mdgdiivfqk ddpndnsel  
781 ptakeyfrdl yhrvdvifcd ktipndpgfv vtlsnrmyf qvaktvaqrl ntdpmlqff  
841 ksqqgyrdgpg nplrhyegt lrdllqffkp rqpkklyyqg lkmkitdfen rrsfkciwln  
901 sqfreeeitl ypdkhgcvr d lleeckkave lgekasgklr lleivsykii gvhgedelle  
961 clspatsrtf rieeipldqv didkenemlv tvahfhkevf gtfgipfllr ihqgefrev  
1021 mkriqslldi qekekfkf aivmtgrhgy inedeyevnl kdfepqpgnm shprpwlgl  
1081 hfnkapkrsr ytlekaiki hn
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8/1/2016 10:06:06 AM

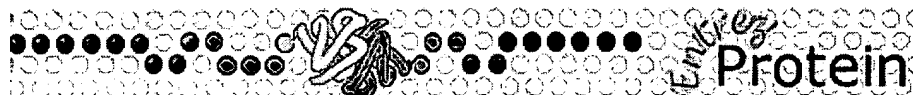
>gi|2501460|sp|Q93009|UBP7_HUMAN Ubiquitin carboxyl-terminal hydrolase 7
(Ubiquitin thiolesterase 7)
(Ubiquitin-specific processing protease 7)
(Deubiquitinating enzyme 7) (Herpesvirus associated
ubiquitin-specific protease)
Length = 1102

Score = 470 bits (1101), Expect = e-132
Identities = 139/139 (100%), Positives = 139/139 (100%)

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Sbjct: 58 DMEDDTSWRSEATFQFTVERFSRLSESVLSPPCFVRNLPWKIMVMMPRFYPDRPHQKSVGF 117

Query: 61 FLQCNAESDSTSWSCHAQAVLKI INYRDDEKSFSRRISHLFFHKENDWGFSNFMWSEVT 120
FLQCNAESDSTSWSCHAQAVLKI INYRDDEKSFSRRISHLFFHKENDWGFSNFMWSEVT
Sbjct: 118 FLQCNAESDSTSWSCHAQAVLKI INYRDDEKSFSRRISHLFFHKENDWGFSNFMWSEVT 177

Query: 121 DPEKGFIDDDKVTFEVQ 139
DPEKGFIDDDKVTFEVQ
Sbjct: 178 DPEKGFIDDDKVTFEVQ 196



Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Books	
Search		Protein	▼	for				Go	Clear
Limits		Preview/Index		History		Clipboard		Details	
Display	default	▼	Show:	20	▼	Send to	File	▼	Get Subsequence

☐ 1: O43791. Speckle-type POZ ...[gi:8134708]

[BLink](#), [Domains](#), [Links](#)

LOCUS O43791 374 aa linear PRI 15-SEP-2003

DEFINITION Speckle-type POZ protein.

ACCESSION O43791

VERSION O43791 GI:8134708

DBSOURCE swissprot: locus SPOP_HUMAN, accession O43791;
class: standard.
created: May 30, 2000.
sequence updated: May 30, 2000.
annotation updated: Sep 15, 2003.
xrefs: gi: 2695707, gi: 2695708, gi: 12654850, gi: 12654851, gi: 13097254, gi: 13097255
xrefs (non-sequence databases): GenewHGNC:11254, MIM 602650, GOGO:0005634, GOGO:0006397, InterProIPR000210, InterProIPR002083, PfamPF00651, PfamPF00917, SMARTSM00225, SMARTSM00061, PROSITEPS50097, PROSITEPS50144

KEYWORDS Antigen; Nuclear protein.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 374)

AUTHORS Nagai,Y., Kojima,T., Muro,Y., Hachiya,T., Nishizawa,Y., Wakabayashi,T. and Hagiwara,M.

TITLE Identification of a novel nuclear speckle-type protein, SPOP

JOURNAL FEBS Lett. 418 (1-2), 23-26 (1997)

MEDLINE 98074898

PUBMED 9414087

REMARK SEQUENCE FROM N.A.

REFERENCE 2 (residues 1 to 374)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S.N., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J.M. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE 22388257

PUBMED 12477932
REMARK SEQUENCE FROM N.A.
TISSUE=Cervix, and Placenta

COMMENT

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[FUNCTION] Antigen recognized by serum from scleroderma patient.
[SUBCELLULAR LOCATION] Nuclear.
[TISSUE SPECIFICITY] Widely expressed.
[SIMILARITY] Contains 1 BTB/POZ domain.
[SIMILARITY] Contains 1 MATH domain.

FEATURES

	Location/Qualifiers
source	1..374 /organism="Homo sapiens" /db_xref="taxon:9606"
gene	1..374 /gene="SPOP"
Protein	1..374 /gene="SPOP"
Region	/product="Speckle-type POZ protein" 31..161 /gene="SPOP" /region_name="Domain" /note="MATH."
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Region	173..297 /gene="SPOP" /region_name="Domain" /note="BTB."

ORIGIN

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181 vpecrladel gglwensrft dcclcvagge fqahkailaa rspvfsamfe hemeeskknr
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361 cpflgpprkr lkqs
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//

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NCBI | NLM | NIH

Seq. 02607076.01

L63 ANSWER 4 OF 4 MEDLINE on STN DUPLICATE 2

ACCESSION NUMBER: 1999239963 MEDLINE

DOCUMENT NUMBER: 99239963 PubMed ID: 10225457

TITLE: Evidence of LMP1-TRAF3 interactions in glycosphingolipid-rich complexes of lymphoblastoid and nasopharyngeal carcinoma cells.

AUTHOR: Ardila-Osorio H; Clausse B; Mishal Z; Wiels J; Tursz T; Busson P

CORPORATE SOURCE: Laboratoire de Biologie des Tumeurs Humaines, UMR 1598 CNRS, Institut Gustave Roussy, Villejuif, France.

SOURCE: INTERNATIONAL JOURNAL OF CANCER, (1999 May 17) 81 (4) 645-9.
Journal code: 0042124. ISSN: 0020-7136.

PUB. COUNTRY: United States

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

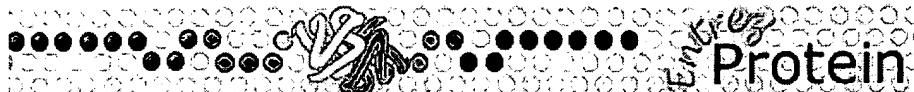
FILE SEGMENT: Priority Journals

ENTRY MONTH: 199905

ENTRY DATE: Entered STN: 19990601
Last Updated on STN: 19990601
Entered Medline: 19990517

AB Latent membrane protein 1 (LMP1) is an Epstein-Barr virus (EBV) protein expressed in EBV-transformed B lymphocytes and in approximately 50% of nasopharyngeal carcinomas (NPCs). LMP1 signaling involves several cellular signaling intermediates, especially TNF receptor-associated factors (TRAFs). We have shown previously that LMP1 is highly concentrated in a cell fraction called glycosphingolipid-rich membrane complexes (GSL complexes). We report here that parallel accumulation of LMP1 and TRAF3, but not TRAF1 or TRADD, was observed in GSL complexes from lymphoblastoid and LMP1-positive NPC cells. In contrast, TRAF3 was not concentrated in GSL complexes from LMP1-negative cells. Binding of LMP1 and TRAF3 in GSL complexes was demonstrated in lymphoblastoid and NPC cells, by co-immunoprecipitation with both anti-LMP1 and **anti-TRAF3** antibodies.

SEQ 8 ✓



Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Book		
Search		Protein	▼	for					Go	Clear
		Limits	Preview/Index		History		Clipboard		Details	
Display	default	▼	Show:	20	▼	Send to	File	▼	Get Subsequence	

☐ 1: Q93009. Ubiquitin carboxy...[gi:2501460]

BLink, Domains, Links

LOCUS Q93009 1102 aa linear PRI 15-SEP-2003
 DEFINITION Ubiquitin carboxyl-terminal hydrolase 7 (Ubiquitin thiolesterase 7) (Ubiquitin-specific processing protease 7) (Deubiquitinating enzyme 7) (Herpesvirus associated ubiquitin-specific protease).
 ACCESSION Q93009
 VERSION Q93009 GI:2501460
 DBSOURCE swissprot: locus UBP7_HUMAN, accession Q93009;
 class: standard.
 created: Nov 1, 1997.
 sequence updated: Nov 1, 1997.
 annotation updated: Sep 15, 2003.
 xrefs: gi: 1545951, gi: 1545952, pdb accession 1NB8, pdb accession 1NBF
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 KEYWORDS Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family; Nuclear protein; 3D-structure.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 1102)
 AUTHORS Everett,R.D., Meredith,M., Orr,A., Cross,A., Kathoria,M. and Parkinson,J.
 TITLE A novel ubiquitin-specific protease is dynamically associated with the PML nuclear domain and binds to a herpesvirus regulatory protein
 JOURNAL EMBO J. 16 (3), 566-577 (1997)
 MEDLINE 97186723
 PUBMED 9034339
 REMARK SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 TISSUE=Breast cancer
 REFERENCE 2 (residues 1 to 1102)
 AUTHORS Everett,R.D., Meredith,M., Orr,A., Cross,A., Kathoria,M. and Parkinson,J.
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 MEDLINE 97277004
 PUBMED 9130697
 REMARK ERRATUM.
 COMMENT

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[SUBCELLULAR LOCATION] NUCLEAR, PRESENT IN A MINORITY OF ND10 NUCLEAR BODIES. ASSOCIATION WITH VMW110 AT EARLY TIMES OF INFECTION LEADS TO AN INCREASED PROPORTION OF HAUSP-CONTAINING ND10.

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[SIMILARITY] Contains 1 MATH domain.

FEATURES	Location/Qualifiers
source	1..1102 /organism="Homo sapiens" /db_xref="taxon:9606"
<u>gene</u>	1..1102 /gene="USP7" /note="synonym: HAUSP"
<u>Protein</u>	1..1102 /gene="USP7" /product="Ubiquitin carboxyl-terminal hydrolase 7" /EC_number="3.1.2.15"
<u>Region</u>	4..10 /gene="USP7" /region_name="Domain" /note="POLY-GLN."
<u>Region</u>	68..195 /gene="USP7" /region_name="Domain" /note="MATH."
<u>Region</u>	201 /gene="USP7" /region_name="Conflict" /note="H -> I (IN REF. 1; AA SEQUENCE)."
<u>Region</u>	205 /gene="USP7" /region_name="Conflict" /note="W -> P (IN REF. 1; AA SEQUENCE)."
<u>Region</u>	207 /gene="USP7" /region_name="Conflict" /note="S -> Q (IN REF. 1; AA SEQUENCE)."
<u>Site</u>	223 /gene="USP7" /site_type="active" /note="BY SIMILARITY."
<u>Site</u>	456 /gene="USP7" /site_type="active" /note="BY SIMILARITY."
<u>Site</u>	464 /gene="USP7" /site_type="active" /note="BY SIMILARITY."
<u>Region</u>	1066 /gene="USP7" /region_name="Conflict" /note="Q -> T (IN REF. 1; AA SEQUENCE)."

ORIGIN

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1-213

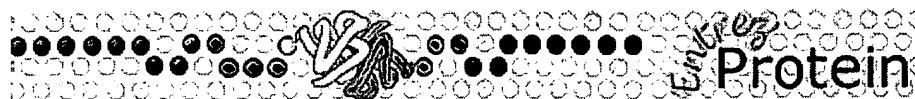
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421 indrfefpeq lpldeflqkt dpkdpanyil havlvhsgdn hgghyvvyln pkgdgkwckf  
481 dddvvsrctk eeaiehnygg hdddlsvrhc tnaymlvyir esklsevlqa vtdhdipqql  
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961 clspatsrtf rieeiPlDQV didkenemlv tvahfhkevf gtfgipfllr ihqgehfrev  
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1081 hfnkapkrsr ytlekaiki hn
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SEQ 25 (mr)



Entrez	PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	Books	
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☐ 1: BAA74921. KIAA0898 protein ...[gi:4240285]

BLink, Links

LOCUS BAA74921 979 aa linear PRI 16-JUN-1999
 DEFINITION KIAA0898 protein [Homo sapiens].
 ACCESSION BAA74921
 VERSION BAA74921.1 GI:4240285
 DBSOURCE accession AB020705.1
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (sites)
 AUTHORS Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirosawa,M.,
 Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.
 TITLE Prediction of the coding sequences of unidentified human genes.
 XII. The complete sequences of 100 new cDNA clones from brain which
 code for large proteins in vitro
 JOURNAL DNA Res. 5 (6), 355-364 (1998)
 MEDLINE 99156230
 PUBMED 10048485
 REFERENCE 2 (residues 1 to 979)
 AUTHORS Ohara,O., Suyama,M., Kikuno,R., Nagase,T. and Ishikawa,K.
 TITLE Direct Submission
 JOURNAL Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research Institute,
 Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
 Fax:+81-438-52-3914)
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181 rnveavrnak dervreirna vemmiarldt qlknklitlm gqktsltqet ellesllqev
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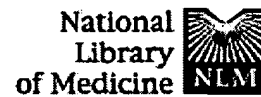
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		Limits	Preview/Index	History	Clipboard	Details				
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☐ 1: Am J Hum Genet. 1997 Apr;60(4):896-902.

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Assignment of the mulibrey nanism gene to 17q by linkage and linkage-disequilibrium analysis.

PubMed Services

Avela K, Lipsanen-Nyman M, Perheentupa J, Wallgren-Pettersson C, Marchand S, Faure S, Sistonen P, de la Chapelle A, Lehesjoki AE.

Department of Medical Genetics, University of Helsinki, Folkhalsan Institute of Genetics, Finland.

Related Resources

Mulibrey nanism (MUL) is an autosomal recessive disorder with unknown basic metabolic defect. It is characterized by growth failure of prenatal onset, characteristic dysmorphic features, constrictive pericardium, hepatomegaly as a consequence of constrictive pericardium, yellowish dots in the ocular fundi, and J-shaped sella turcica. Hypoplasia of various endocrine glands, causing hormone deficiencies, is common. Here we report the assignment of the MUL gene, by linkage analysis in Finnish families, to a 7-cM region flanked by D17S1799 and D17S948 on chromosome 17q. Multipoint linkage analysis gave a maximum LOD score of 5.01 at loci D17S1606-D17S1853 and at D17S1604. The estimate of the critical MUL region was further narrowed to within approximately 250 kb of marker D17S1853 by linkage disequilibrium analysis. Positional candidate genes that belong to the growth hormone and homeobox B gene clusters were excluded. These data confirm the autosomal recessive inheritance of MUL and allow highly focused attempts to clone the gene.

MeSH Terms:

- Abnormalities, Multiple/epidemiology
- Abnormalities, Multiple/genetics*
- Brain/abnormalities
- Chromosome Mapping
- Chromosomes, Human, Pair 17/genetics*
- Dwarfism/epidemiology
- Dwarfism/genetics*
- Eye Abnormalities/genetics
- Female
- Finland/epidemiology
- Genes, Recessive*

- Genetic Markers
- Homeodomain Proteins/genetics
- Human
- Linkage Disequilibrium
- Liver/abnormalities
- Lod Score
- Male
- Microsatellite Repeats
- Muscles/abnormalities
- Polymorphism (Genetics)
- Recombination, Genetic
- Support, Non-U.S. Gov't

Substances:

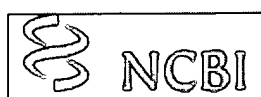
- Genetic Markers
- Homeodomain Proteins

PMID: 9106536 [PubMed - indexed for MEDLINE]

Display	Citation	▼	Show:	20	▼	Sort	▼	Send to	Text	▼
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Nov 3 2009 06:32:01



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		Limits	Preview/Index	History	Clipboard	Details			
Display	default	▼	Show:	20	▼	Send to	File	▼	Get Subsequence

☐ 1: NP_932104. tripartite motif ...[gi:37574064]

BLink, Links

LOCUS NP_932104 961 aa linear ROD 29-OCT-2003
DEFINITION tripartite motif protein 37 [Mus musculus].
ACCESSION NP_932104
VERSION NP_932104.1 GI:37574064
DBSOURCE REFSEQ: accession NM_197987.1
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (residues 1 to 961)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnierch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE 22388257
PUBMED 12477932
REFERENCE 2 (residues 1 to 961)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C.,
Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H.,
Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V.,
Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A.,
Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T.,
Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A.,
Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R.,
Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S.,
Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M.,

Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420 (6915), 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
REFERENCE 3 (residues 1 to 961)
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 4 (residues 1 to 961)
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K. and Togawa,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 5 (residues 1 to 961)
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 6 (residues 1 to 961)
AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 7 (residues 1 to 961)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final NCBI review. The reference sequence was derived from BC058678.1.

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L13 ANSWER 7 OF 18 MEDLINE on STN

ACCESSION NUMBER: 1998088906 MEDLINE

DOCUMENT NUMBER: 98088906 PubMed ID: 9428630

TITLE: NotI linking/jumping clones of human chromosome 3: mapping of the TFRC, RAB7 and **HAUSP** genes to regions rearranged in leukemia and deleted in solid tumors.

AUTHOR: Kashuba V I; Gizatullin R Z; Protopopov A I; Allikmets R; Korolev S; Li J; Boldog F; Tory K; Zabarovska V; Marcsek Z; Sumegi J; Klein G; Zabarovsky E R; Kisselev L

CORPORATE SOURCE: Microbiology and Tumor Biology Center, Karolinska Institute, Stockholm, Sweden.

SOURCE: FEBS LETTERS, (1997 Dec 15) 419 (2-3) 181-5.
Journal code: 0155157. ISSN: 0014-5793.

PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

OTHER SOURCE: GENBANK-Z22474; GENBANK-Z94768

ENTRY MONTH: 199801

ENTRY DATE: Entered STN: 19980206
Last Updated on STN: 20000303
Entered Medline: 19980127

AB By applying the 'recognition mask' strategy to 300 mammalian sequences containing NotI sites we demonstrated that 5' ends of genes are highly enriched in NotI sites. A NotI linking clone NL2-252 (D3S1678) containing transferrin receptor (TFRC) gene was used as an initial point for chromosomal jumping. One of the jumping clones, J21-045 traverses 210 kbp and links NL2-252 to NL26 (D3S1632), a NotI linking clone containing highly polymorphic sequences. The TFRC gene was mapped to 3q29, close to the telomeric marker D3S2344, by linkage analysis, a panel of hybrid cell lines, GeneBridge 4 panel and FISH. Clone NLM-007 (D3S4302) was found to contain ras-homologous gene RAB7. By FISH and a panel of hybrid cell lines this gene was mapped to 3q21. This region is of particular interest due to frequent rearrangements in different types of leukemia. Clone L2-081 (D3S4283) containing new member of ubiquitin-specific proteases (**HAUSP** gene) was localized in 3p21 inspiring further investigation of involvement of this gene in development of lung and renal carcinomas.

L46 ANSWER 14 OF 28 LIFESCI COPYRIGHT 2003 CSA on STN

ACCESSION NUMBER: 2000:7058 LIFESCI

TITLE: TRAF2 Deficiency Results in Hyperactivity of Certain TNFR1
Signals and Impairment of CD40-Mediated Responses

AUTHOR: Nguyen, L.T.; Duncan, G.S.; Mirtsos, C.; Ng, M.; Speiser,
D.E.; Shahinian, A.; Marino, M.W.; Mak, T.W.; Ohashi, P.S.;
Yeh, W.-C.

CORPORATE SOURCE: Amgen Institute, Ontario Cancer Institute, Toronto,
Ontario, Canada M5G 2C1; E-mail: wen-chen.yeh@amgen.com

SOURCE: Immunity, (19990900) vol. 11, no. 3, pp. 379-389.
ISSN: 1074-7613.

DOCUMENT TYPE: Journal

FILE SEGMENT: F

LANGUAGE: English

SUMMARY LANGUAGE: English



L46 ANSWER 11 OF 28 CANCERLIT on STN

ACCESSION NUMBER: 1999239963 CANCERLIT
DOCUMENT NUMBER: 99239963 PubMed ID: 10225457
TITLE: Evidence of LMP1-TRAF3 interactions in glycosphingolipid-rich complexes of lymphoblastoid and nasopharyngeal carcinoma cells.
AUTHOR: Ardila-Osorio H; Clausse B; Mishal Z; Wiels J; Tursz T; Busson P
CORPORATE SOURCE: Laboratoire de Biologie des Tumeurs Humaines, UMR 1598 CNRS, Institut Gustave Roussy, Villejuif, France.
SOURCE: INTERNATIONAL JOURNAL OF CANCER, (1999 May 17) 81 (4) 645-9.
Journal code: 0042124. ISSN: 0020-7136.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: MEDLINE; Priority Journals
OTHER SOURCE: MEDLINE 1999239963
ENTRY MONTH: 199905
ENTRY DATE: Entered STN: 19990622
Last Updated on STN: 19990622

AB Latent membrane protein 1 (LMP1) is an Epstein-Barr virus (EBV) protein expressed in EBV-transformed B lymphocytes and in approximately 50% of nasopharyngeal carcinomas (NPCs). LMP1 signaling involves several cellular signaling intermediates, especially **TNF receptor-associated factors** (TRAFs). We have shown previously that LMP1 is highly concentrated in a cell fraction called glycosphingolipid-rich membrane complexes (GSL complexes). We report here that parallel accumulation of LMP1 and TRAF3, but not TRAF1 or TRADD, was observed in GSL complexes from lymphoblastoid and LMP1-positive NPC cells. In contrast, TRAF3 was not concentrated in GSL complexes from LMP1-negative cells. Binding of LMP1 and TRAF3 in GSL complexes was demonstrated in lymphoblastoid and NPC cells, by co-immunoprecipitation with both anti-LMP1 and anti-TRAF3 **antibodies**.